

FIG. 2

3/34

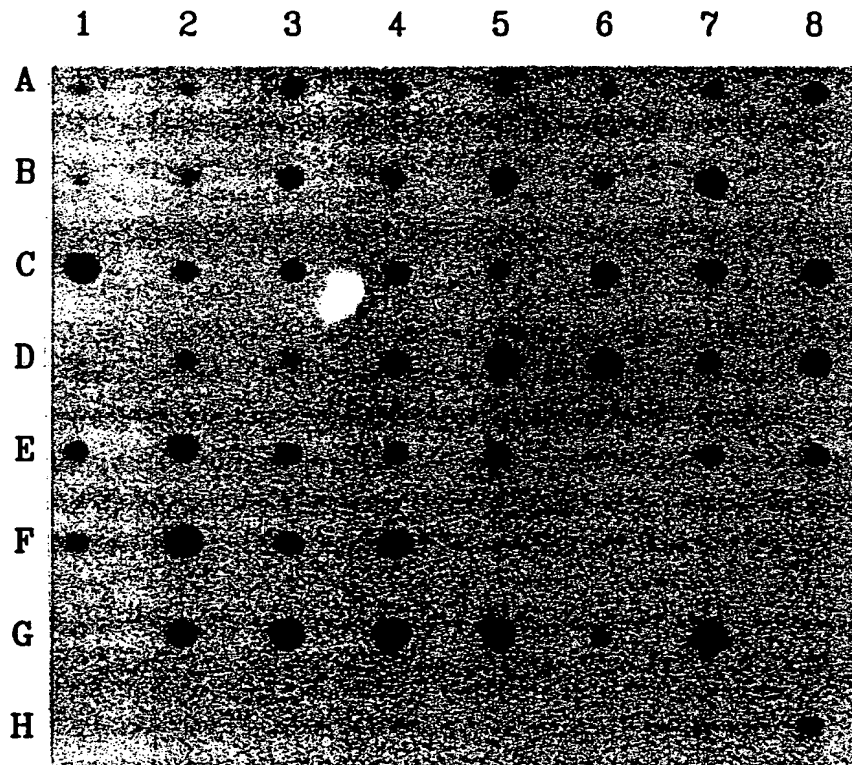


FIG. 3

4/34

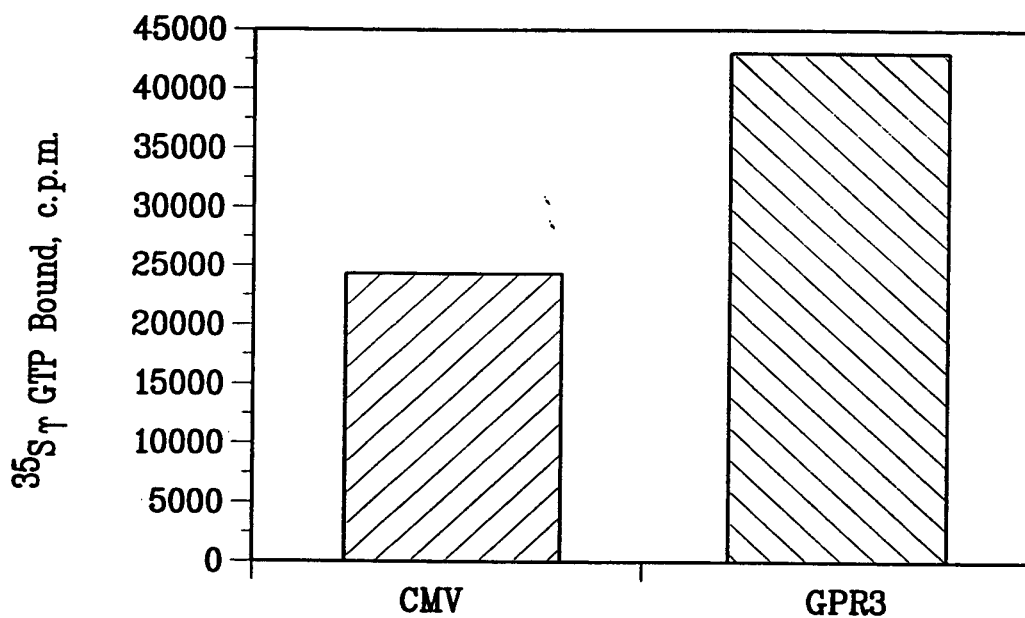


FIG. 4

Figure 5A

10 30 40

1 M H - - - - - W G A G S SEQ.ID.NO.: 46
1 M N A S A A S L N D S Q V V V V A A E G A A A A A T A A G G P D T G E W G P P A SEQ.ID.NO.: 47
1 M N - - - - - E D L K V N L - - - - - S G L SEQ.ID.NO.: 48

50 60 70 80

8 P L A W L S I A G S G N V N V S S V G P A E G P T G P A A P L P S P K A W D V V L SEQ.ID.NO.: 46
41 A A A - L G A G G G A N G S L E L S S Q L S A G P P G L L L P A V N P W D V L L SEQ.ID.NO.: 47
13 P R D Y L D A A A A E N I S A A V S S R V P A V E P E P E L - V N N P W D I V L SEQ.ID.NO.: 48

90 100 110 120

48 C I S G T L V S C E N A L V V A I I V G T P A F R A P M F L L V G S L A V A D L SEQ.ID.NO.: 46
80 C V S G T V I A G E N A L V V A L I A S T P A L R T P M F V L V G S L A T A D L SEQ.ID.NO.: 47
52 C T S G T L I S C E N A I V V L I I F H N P S L R A P M F L L I G S L A L A D L SEQ.ID.NO.: 48

130 140 150 160

88 L A G L G L V L H F A A V F C I G S A E H S L V L V G V L A M A F T A S I G S L SEQ.ID.NO.: 46
120 L A G C G L I L H F V F Q Y L V P S E T V S L L T V G F L V A S F A A S V S S L SEQ.ID.NO.: 47
92 L A G I G L I T N F V F A Y L L Q S E A T K L V T I G L I V A S F S A S V C S L SEQ.ID.NO.: 48

170 180 190 200

128 L A I T V D R Y L S L Y N A L T Y Y S E T T V T R T Y V M L A L V W G G A L G L SEQ.ID.NO.: 46
160 L A I T V D R Y L S L Y N A L T Y Y S R R T L L G V H L L L A A T W T V S L G L SEQ.ID.NO.: 47
132 L A I T V D R Y L S L Y Y A L T Y H S E R T V T F T Y V M L V M L W G T S I C L SEQ.ID.NO.: 48

210 220 230 240

168 G L L P V L A W N C L D G L T T C G V V Y P L S K N H L V V L A I A F F M V F G SEQ.ID.NO.: 46
200 G L L P V L G W N C L A E R A A C S V V R P L A R S H V A L L S A A F F M V F G SEQ.ID.NO.: 47
172 G L L P V M G W N C L R D E S T C S V V R P L T K N N A A I L S V S F L F M F A SEQ.ID.NO.: 48

250 260 270 280

208 I M L Q L Y A Q I C R I V C R H A Q Q I A L Q R H L L P A S H Y V A T R K G I A SEQ.ID.NO.: 46
240 I M L H L Y V R I C Q V V W R H A H Q I A L Q Q H C L A P P H L A A T R K G V G SEQ.ID.NO.: 47
212 L M L Q L Y I Q I C K I V M R H A H Q I A L Q H H F L A T S H Y V T T R K G V S SEQ.ID.NO.: 48

290 300 310 320

248 T L A V V L G A F A A C W L P F T V Y C L L G D A H S P P L Y L T L L P A T SEQ.ID.NO.: 46
280 T L A V V L G T F G A S W L P F A I Y C V V G S H E D P A V Y T Y A T L L P A T SEQ.ID.NO.: 47
252 T L A I I L G T F A A C W M P F T L Y S L I A D Y T Y P S I Y T Y A T L L P A T SEQ.ID.NO.: 48

330 340 350 360

288 Y N S M I N P I I Y A F R N Q D V Q K V L W A V C C C C S S S K I P F F R S R S P SEQ.ID.NO.: 46
320 Y N S M I N P I I Y A F R N Q E I Q R A L W L L L C G C F Q S K V P F F R S R S P SEQ.ID.NO.: 47
292 Y N S I I N P V I Y A F R N Q E I Q K A L C L I C C G C I P S S L A Q R A R S P SEQ.ID.NO.: 48

328 S D V SEQ.ID.NO.: 46
360 S E V SEQ.ID.NO.: 47
332 S D V SEQ.ID.NO.: 48

Figure 5B

	10	20	30	40					
1	MNESRWTEWRI	LNMS SGIV	NVSE RHS	CPLGFGHYSVVDVC	SEQ.ID.NO.: 19				
1	MNST - - - - -	LD - - - - -	GNS SHPF	CLLAFGY - - - - -	SEQ.ID.NO.: 15				
	50	60	70	80					
41	IFETV VIV	LLTFLII	-----	AGNLT VIFVFHCAPLLH	SEQ.ID.NO.: 19				
22	- LETV NFC	LLEVLII	VFLT VLIIS	GNII VIFVFHCAPLL	SEQ.ID.NO.: 15				
	90	100	110	120					
73	HYTTSYFIQT	MAYADLFVGVSC	LVPTLSLLH	YSTGVHESL	SEQ.ID.NO.: 19				
61	HTTTSYFIQT	MAYADLFVGVSC	VVPSSL	LLHHPLPVEESL	SEQ.ID.NO.: 15				
	130	140	150	160					
113	TCQVFGYII	SVLKSVSMA	CLACISV	DRYL AITKPLSYNQL	SEQ.ID.NO.: 19				
101	TCQIFGFVV	SVLKSVSMA	S LACISIDRYI	AITKPLTYNTL	SEQ.ID.NO.: 15				
	170	180	190	200					
153	VTPCRLRI	CILIIWIIYS	CLIFLPSFF	GWGKPGYHGDIFEW	SEQ.ID.NO.: 19				
141	VTFWRRLRL	CIFLIIWL	YSTLVFLPSFF	HWGKPGYHGDVFW	SEQ.ID.NO.: 15				
	210	220	230	240					
193	CATSWLTS	AYFTGFIV	CLYAPAA	FVVCFTYFHI	FKICRQ	SEQ.ID.NO.: 19			
181	CAESWHT	DSYFTL	LFIVMM	LYAPAA	LI VCFYFNIFRIC	SEQ.ID.NO.: 15			
	250	260	270	280					
233	HTKEIN	DRRARFP	SHVEDSS	RETGHSP	DRRYAMVLF	FRITS	SEQ.ID.NO.: 19		
221	HTKD	ISERQ	ARFS	SQSGETG	- EVQAC	PKRYAMVLF	FRITS	SEQ.ID.NO.: 15	
	290	300	310	320					
273	VFYML	WLPIIYFL	LESS	RVLDN	NPTLS	SFLT	TWLAISNS	SFC	SEQ.ID.NO.: 19
260	VFYI	WLPIIY	FLLESS	TGHSN	RFA	SFLT	TWLAISNS	SFC	SEQ.ID.NO.: 15
	330	340	350	360					
313	NCVIYSL	SNVFR	RLGLRRL	SETMCT	SCMCVKDQE	AQEP	- -	SEQ.ID.NO.: 19	
300	NCVIYSL	SNVFOR	GLKRLS	GAMCT	SC - -	ASQTT	ANDPYT	SEQ.ID.NO.: 15	
	370								
351	- KPRKRA	NSCSI							SEQ.ID.NO.: 19
338	VRSKGPL	NGCHI							SEQ.ID.NO.: 15

7/34

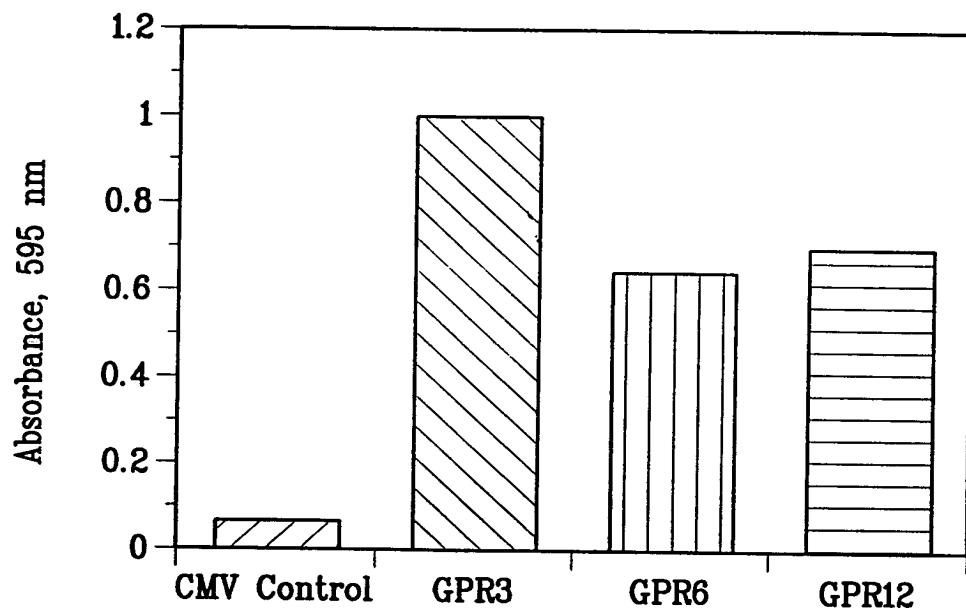


FIG. 6A

8/34

FIG. 6B

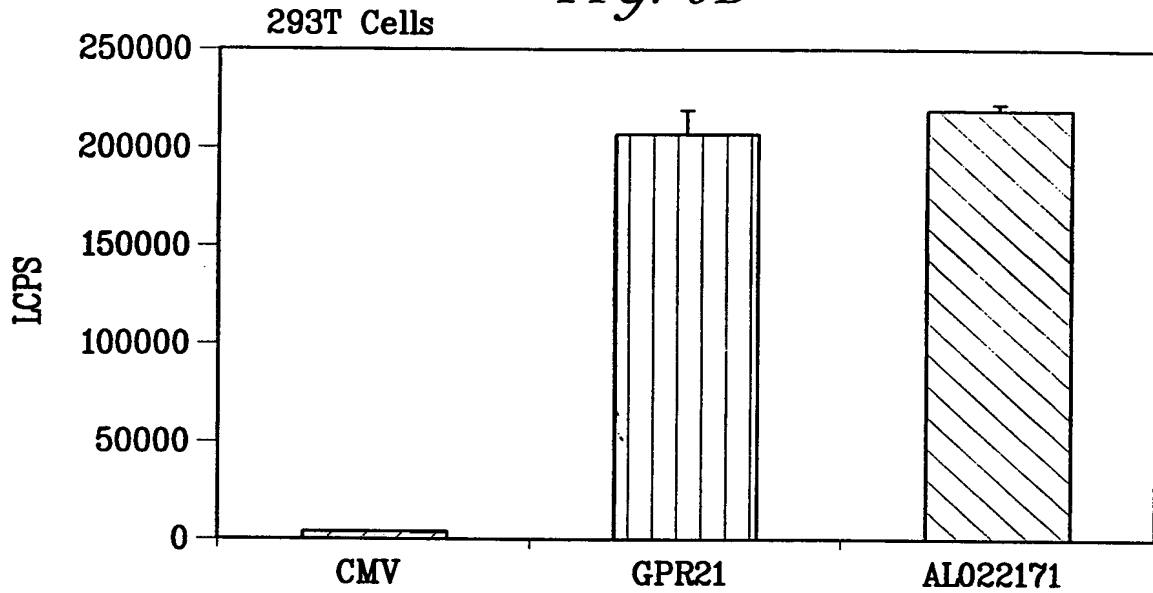
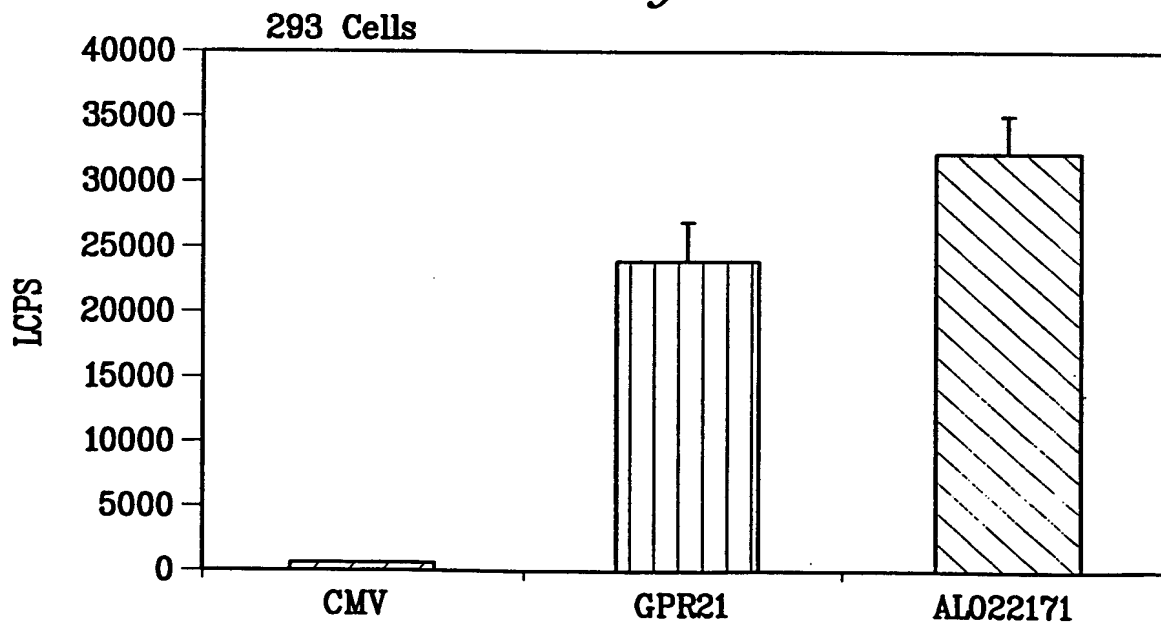
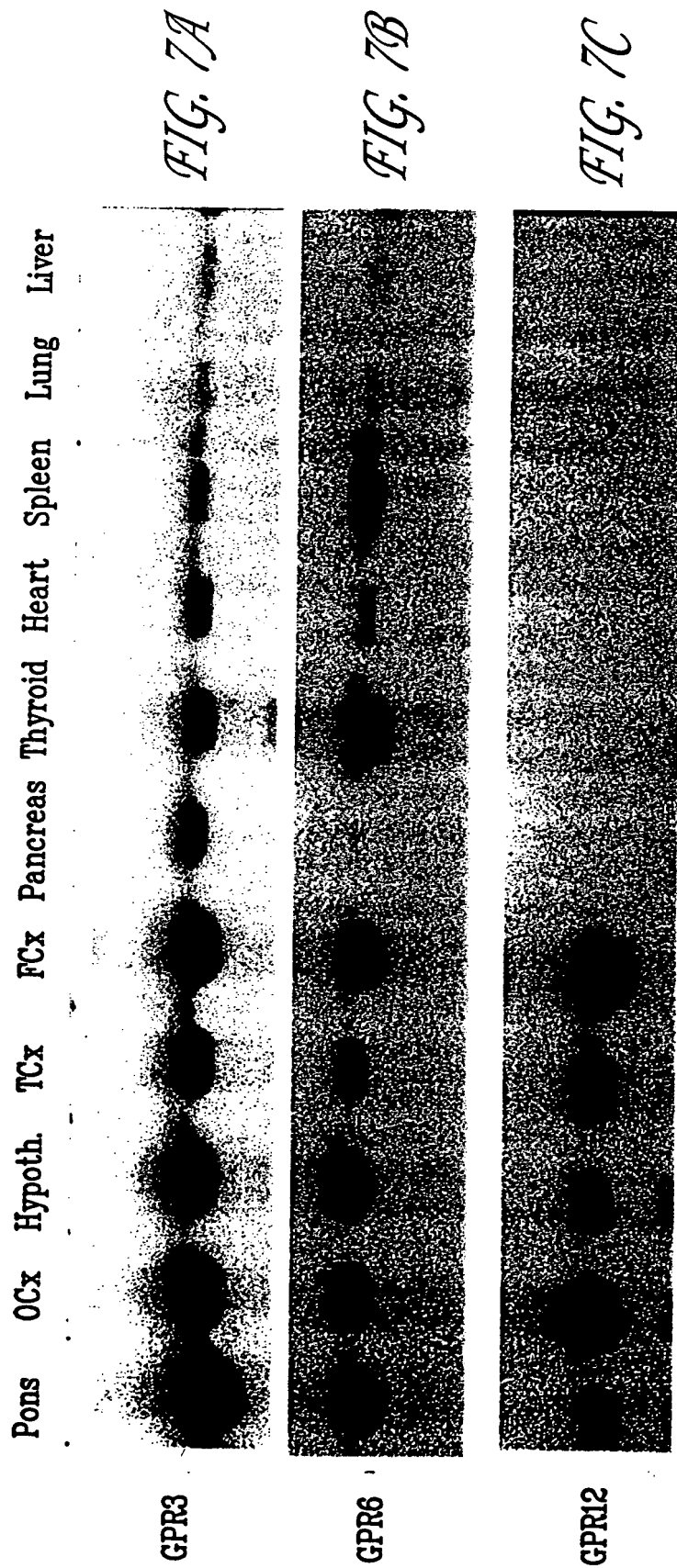


FIG. 6C

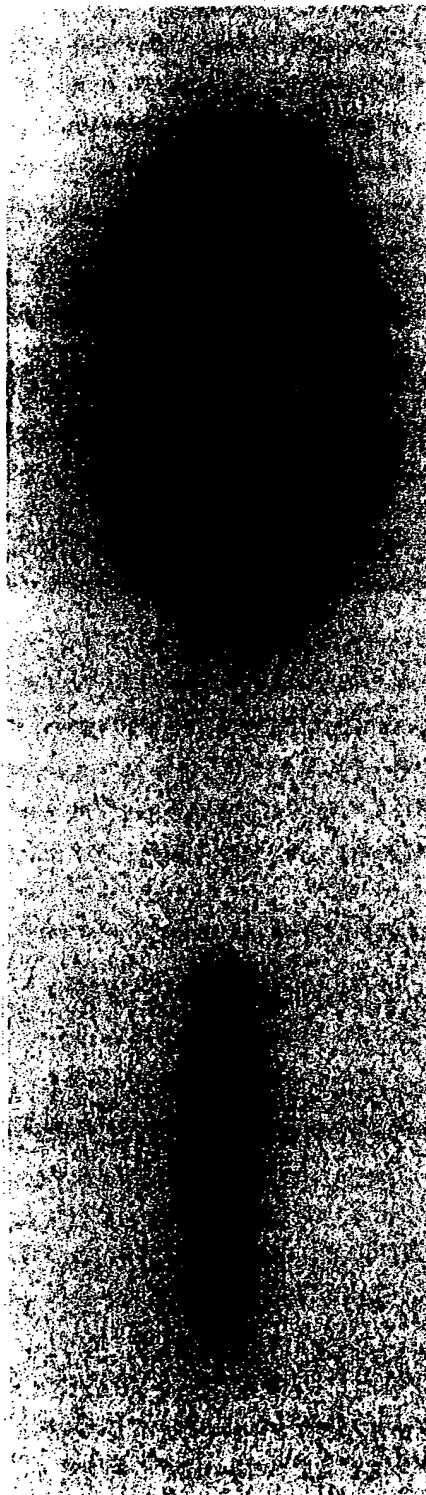


9/34



10/34

FIG. 8

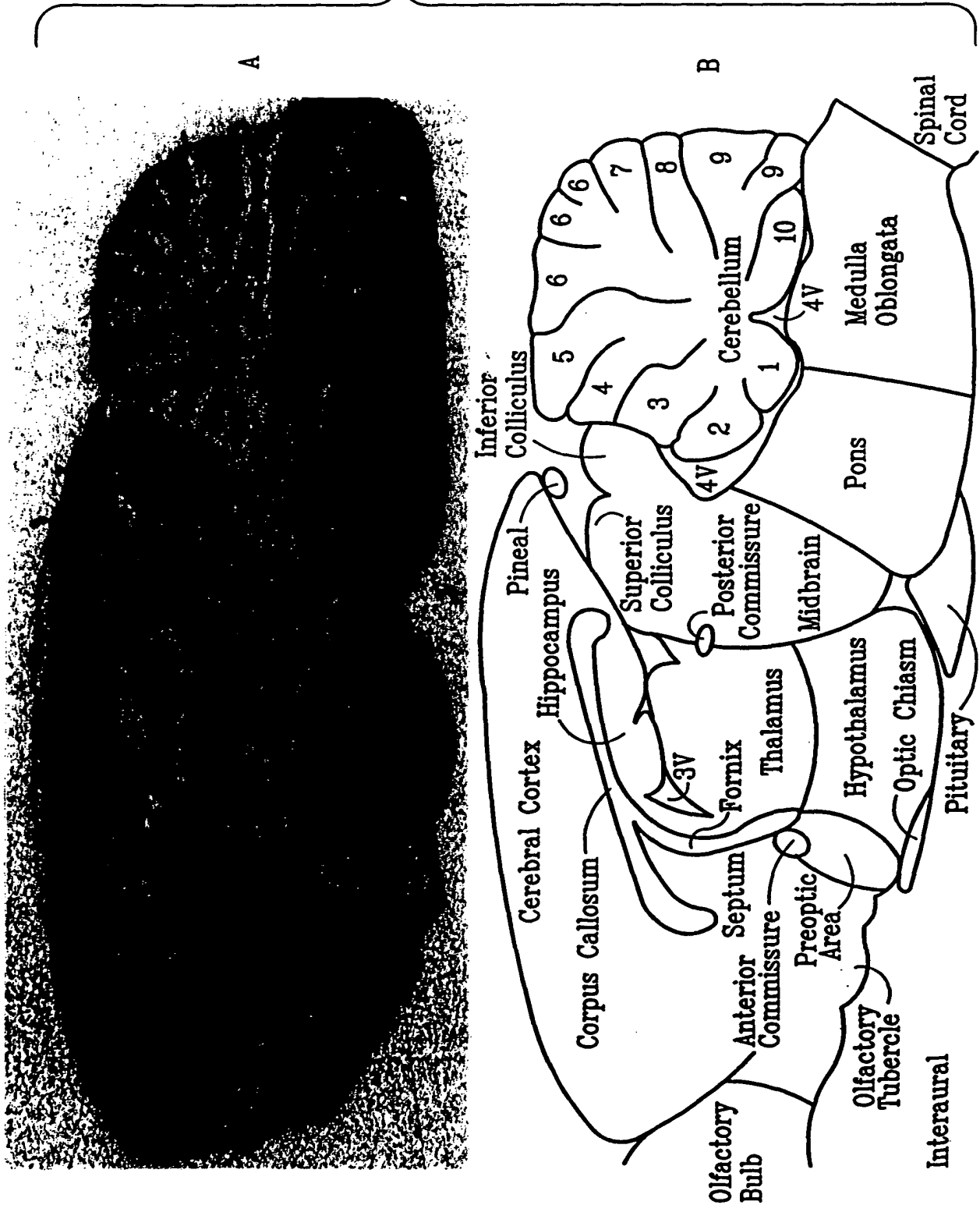


Control Tissue
A

Epilepsy Biopsy
B

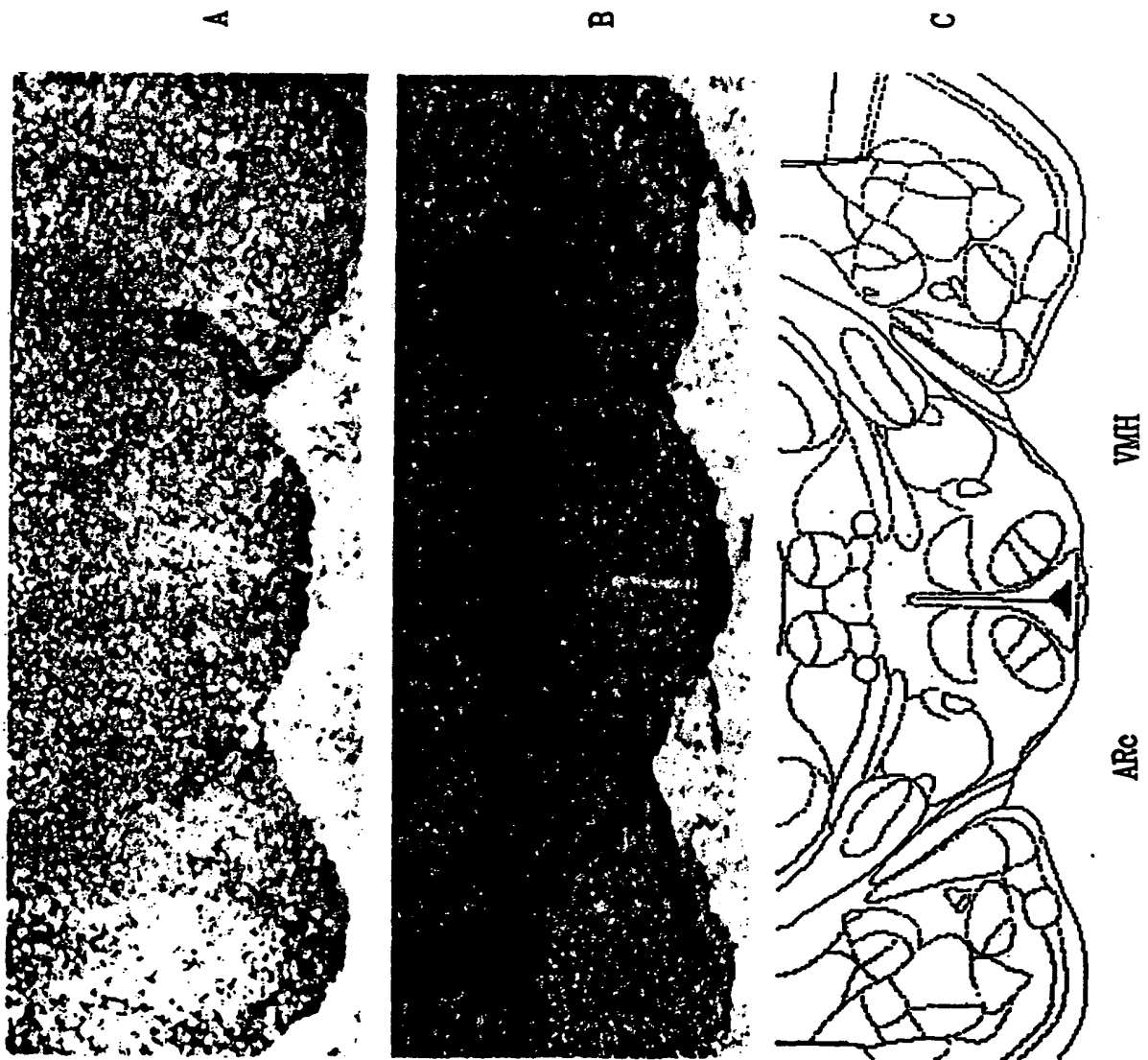
FIG. 9

11/34



12/34

FIG. 10



13/34

FIG. 11B



FIG. 11A



14/34

FIG. 11D

Hippocampus



Cortical Amygdaloid
Nucleus



FIG. 11C

Frontal Cortex



Lateral Septum

FIG. 11E

Lateral Septum

15/34

FIG. 11F

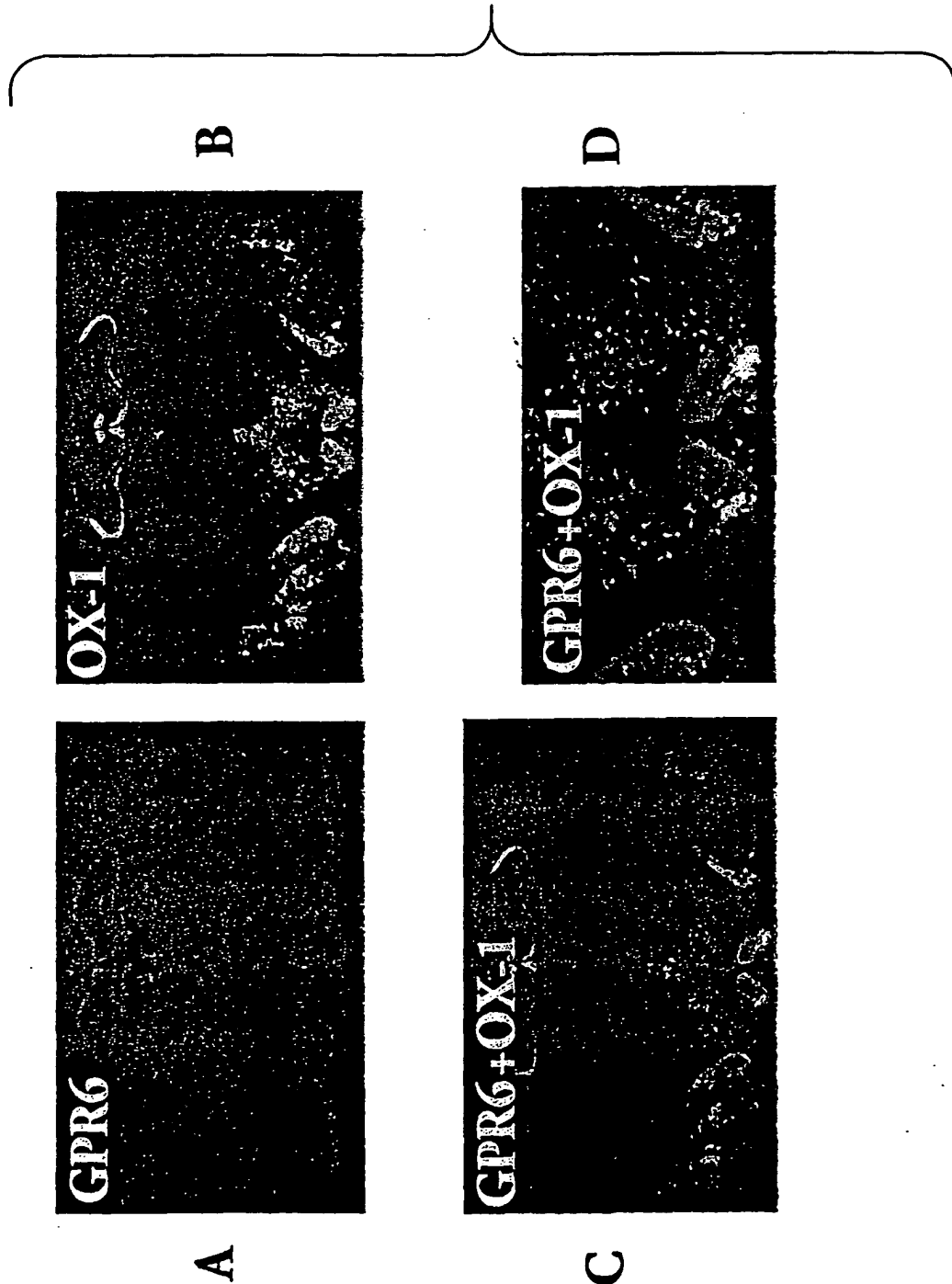


VTA

Substantia Nigra
(compacta)

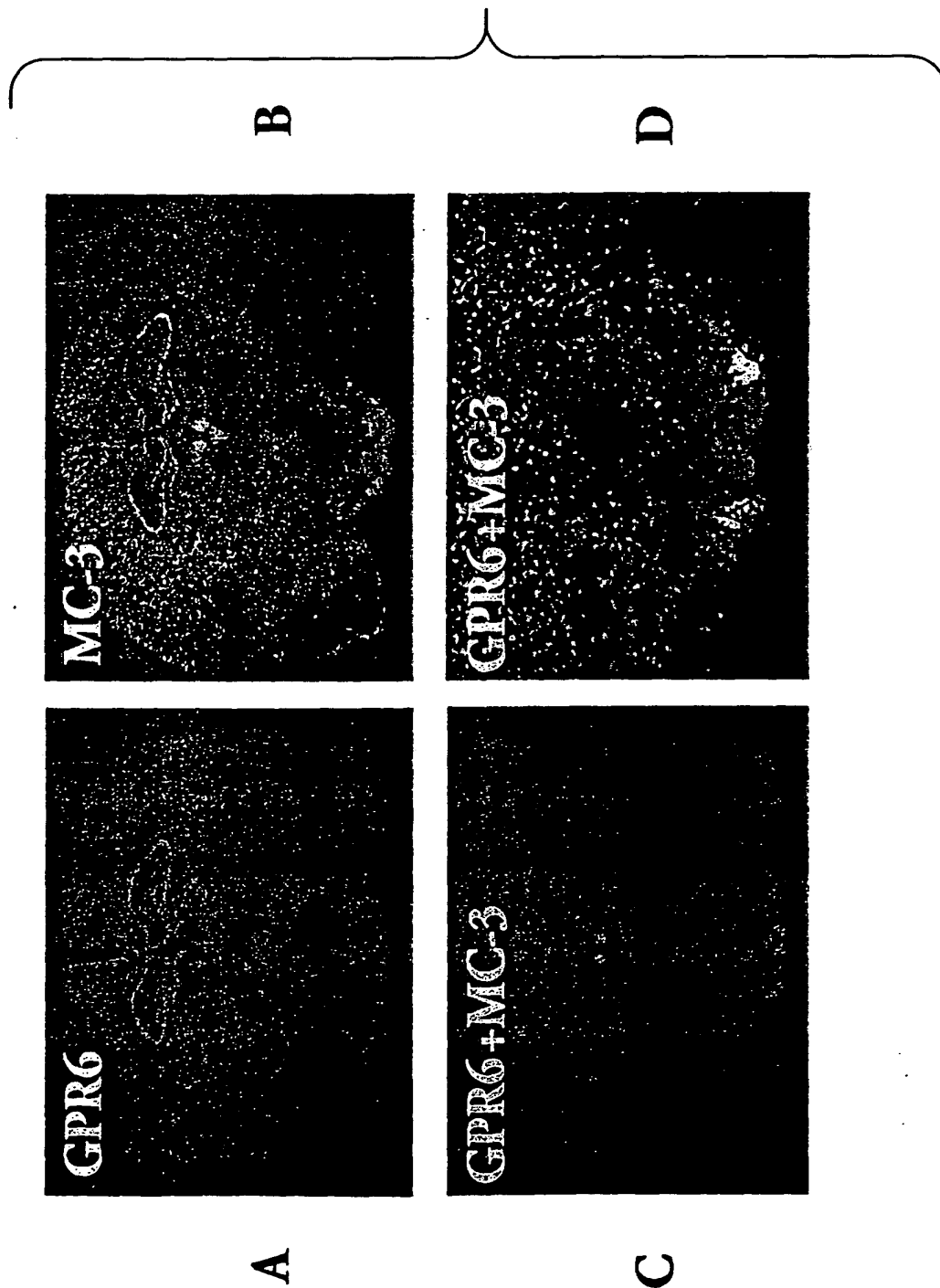
16/34

FIG. 12



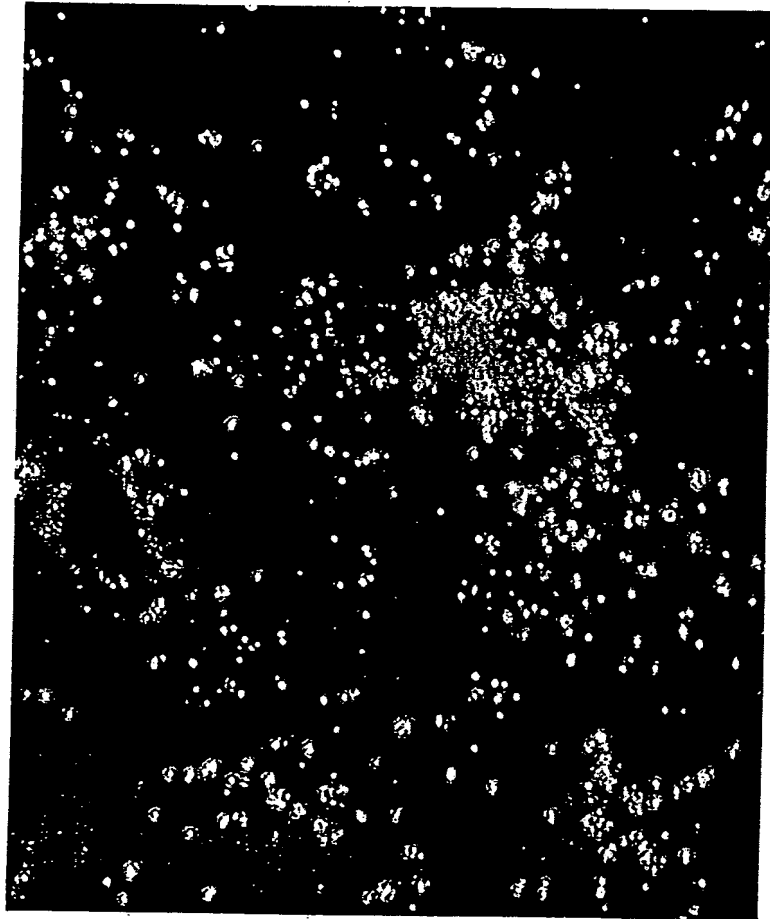
17/34

FIG. 13



18/34

FIG. 14



19/34

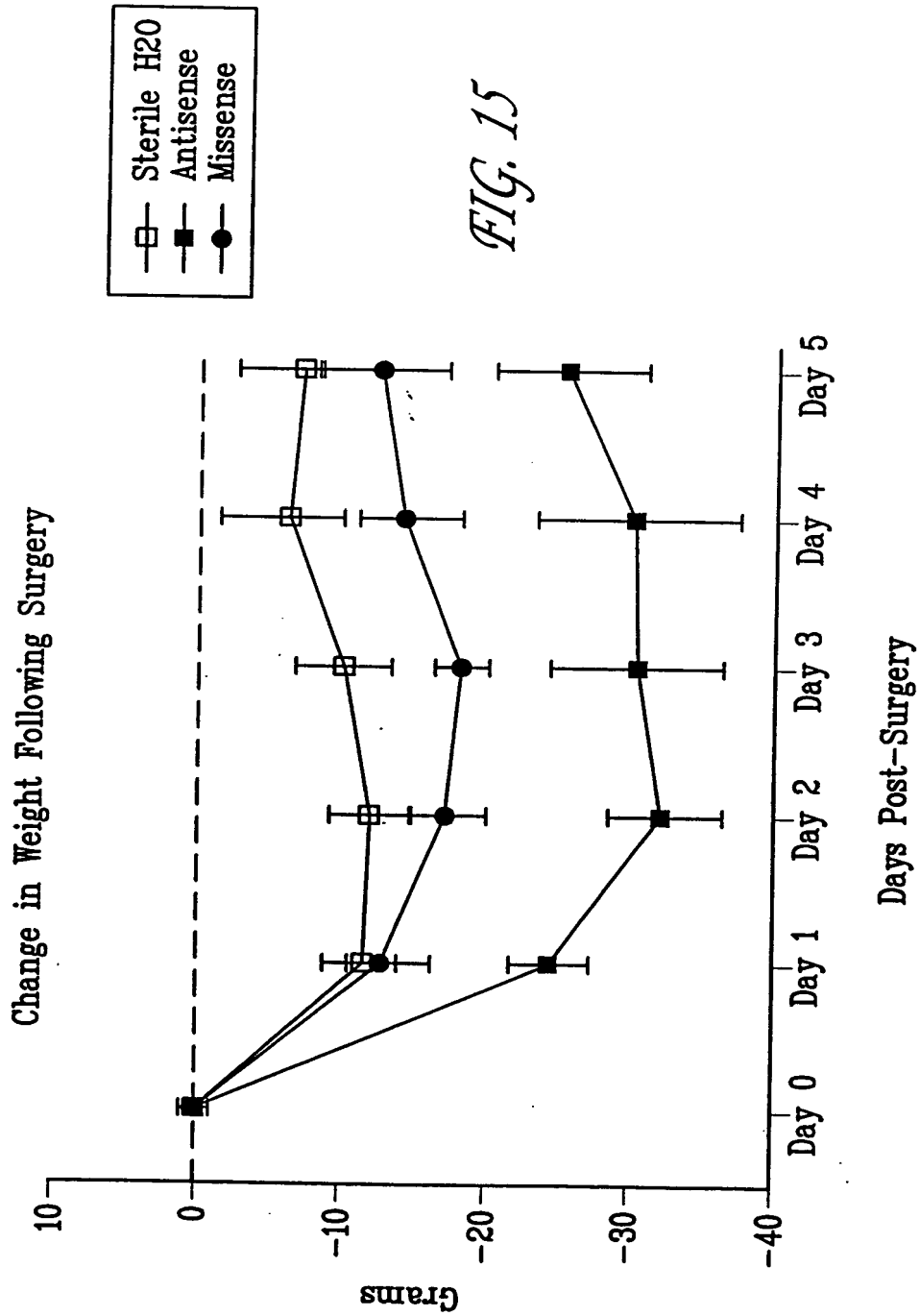
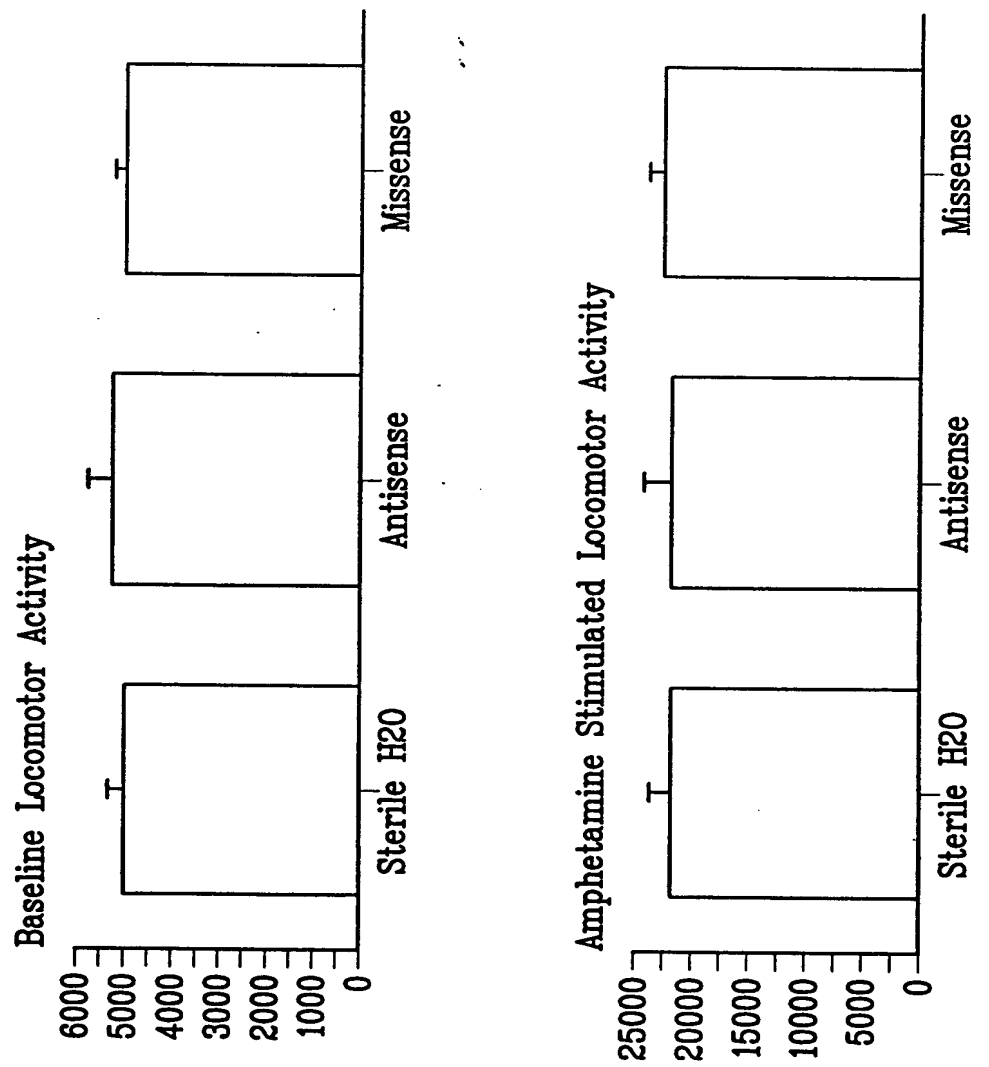


FIG. 16



21/34



FIG. 17A

23/34

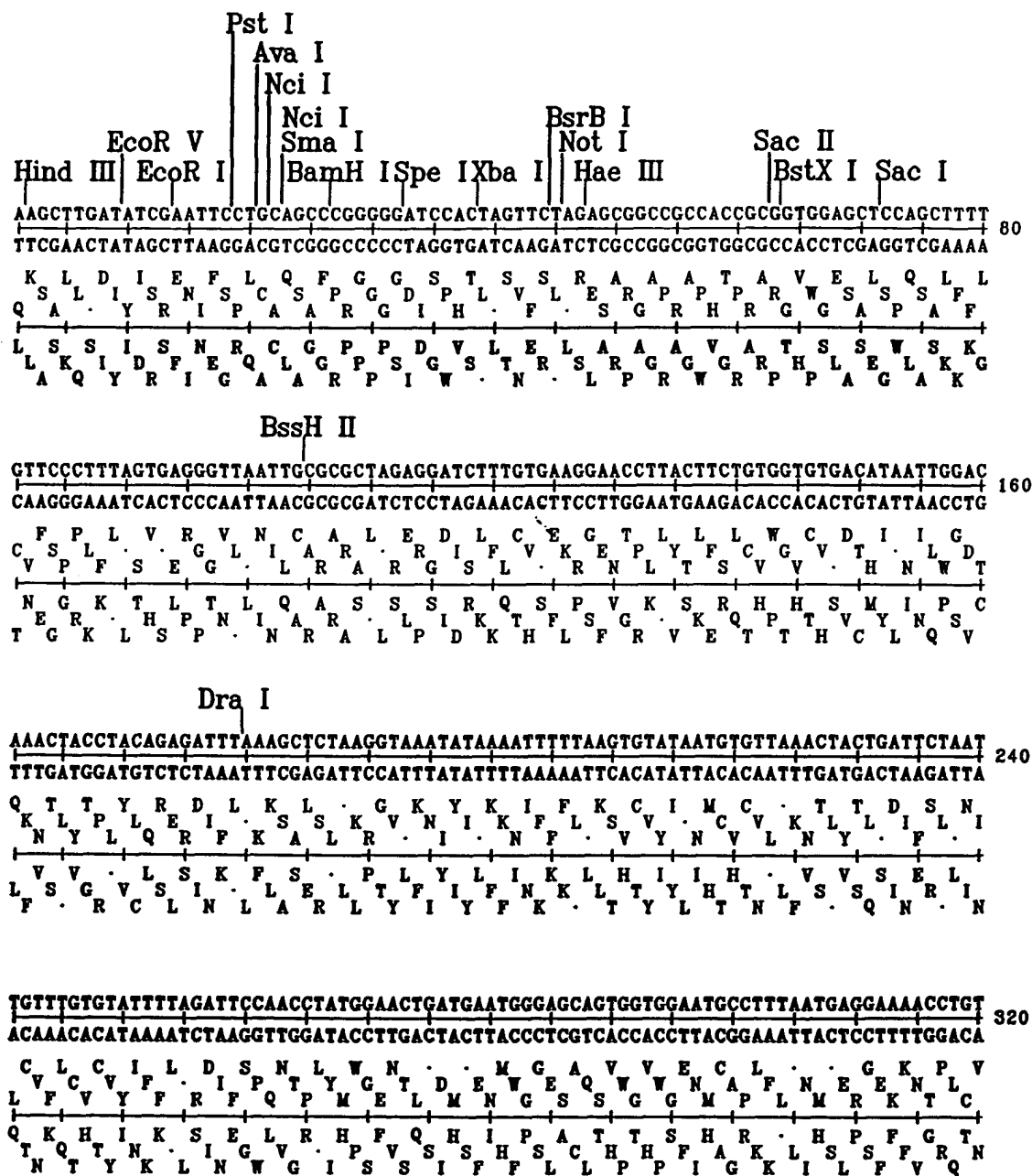


FIG. 18A

24/34

TTTGCTCAGAAGAAATGCCATCTAGTGATGATGAGGCTACTGCTGACTCTCAACATTCTACTCCTCCAAAAAAGAAGAGA 400
AAACGAGTCTTCTTTACGGTAGATCACTACTCTCCGATGACGACTGAGAGTTGTAAGATGAGGAGGTTTTTCTTCTCT
L L R R N A I G Y C L S T F Y S S K K E E
F C A Q K K C H L V M M R A L L T L N I L L Q K K R R E
K S L L F A M H H H P Q Q S E V N E E L F S S F
K Q E S S I G D L S S S A V A S E C E V G G F F L L S
K A F F H W R T I I L S S S V R L M R S R W F F L L S

Sty I

AAGGTAGAAGACCCCAAGGACTTTCCTTCAGAATTGCTAAGTTTTTGAATCATGCTGTGTTTAGTAATAGAAGTCTTGC 480
TTCCATCTTCTGGGGTTCCTGAAAGGAAGTCTTAACGATTCAAAAACTCAGTACGACACAAATCATTATCTTGAGAAGC
K G R R P Q G L S F R I A K F F E S C C V N S C
K V E D P K D F P S E L L S F L S H A V F S N R T L L A
R K T P R T F L Q N C V F V M L C L V I E L L
F L L G W P S E K L I A L N K S D H Q T Y Y F E R Q
L T S F V G L S V K G E S N S L K K L A T H N L L V S R A
L Y F V G L S V K R F Q T K Q T M S H K T I S S K S

TTGCTTTGCTATTTACACCACAAAGGAAAAAGCTGCACTGCTATACAAGAAATTTATGGAAAAATATTCTGTAACCTTTA 560
AACGAAACGATAAATGTGGTGTTCCTTTTTTCGACGTGACGATATGTTCTTTTAATACCTTTTTATAAGACATTGGAAAT
L L C Y L H H K G K S C T A I Q E N Y G K I F C N L Y
L C F A I Y T T K E K A A L L Y K K I M E K K Y S V T F L
L A L L F T P Q R K K L H C Y T R K L W K N I L P L
K S Q K C W L P F L Q V A I C S F P F I N Q L R I
Q K A I V V F S F A A S S Y L F I I S F F Y E T V K I
A K S N V G C L F F S C Q V L F N H F F I R Y G K I

AseI

TAAGTAGGCATAACAGTTATAATCATAACTGTTTTTCTTACTCCACACAGGCATAGAGTGTCTGTATTAATAAC 640
ATTCATCCGTATTGTCAATATTAGTATTGTATGACAAAAAGAATGAGGTGTGTCCTATCTCACAGACGATAATTATG
K A Q L S H T V F S Y S T Q A S V C Y
I S R H N S Y N H N I L F F L T P H R H R V S A I N N
V G I T V I I Y Y C F F L L H T G I E C L L L I T
L Y A Y C N Y D Y C V T K E E V C A Y L T D Q I L L S
Y T P M V T I I M V Y S N K K K S W V P M S H R S I N I V

Rsa I

TATGCTCAAAAATTGTGTACCTTTAGCTTTTTAATTTGTAAAGGGGTTAATAAGGAATATTTGATGTATAGTGCCCTTGAC 720
ATACGAGTTTTTAACACATGGAAATCGAAAAATTAACATTTCCTTAATAACTACATATCACGGAAGT
L C S K I V Y L L F N L R G G I F D Y C L D
Y A Q K L C T P L S F L I C K G V N K E Y L M Y S A L T
M L K N C V P L A F F V K G L I R N I C I V P
H E F I T Y R S K L K Y L P Y P I N S T Y H R S V
I A L F N H V K L K K I Q L P T L L S Y I K I Y L A K V
I S L F Q T G K A K N T F P N I L F I Q H I T G Q V S

FIG. 18B

FIG. 18C

26/34

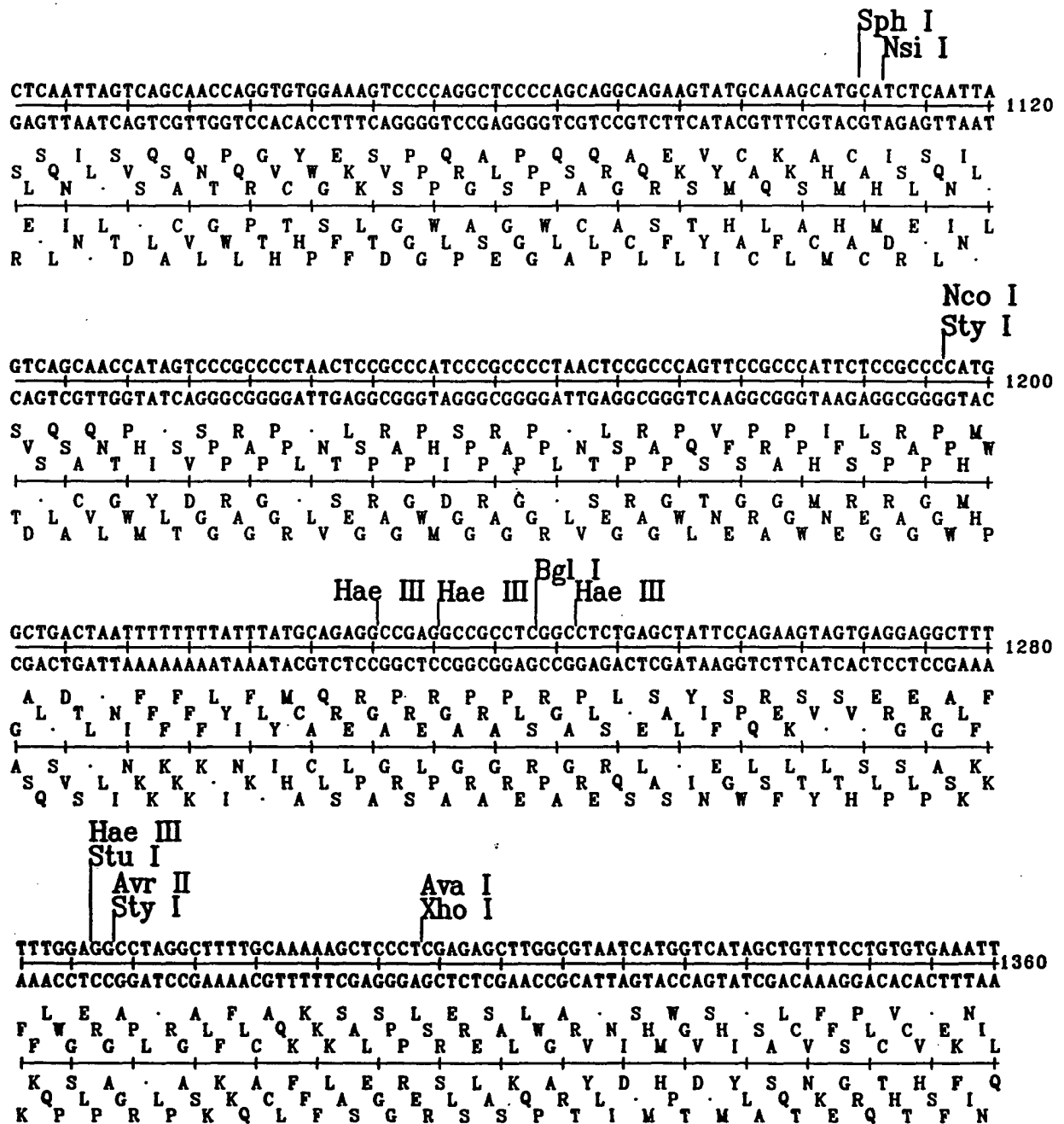


FIG. 18D

27/34

BsrB I

GTTATCCGCTCACAAATTCACACAACATACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAA 1440
CAATAGGCGAGTGTTAAGGTGTGTTGTATGCTCGGCCTTCGTATTTACATTTDGGACCCACGGATTACTCACTCGATT
C Y P L T I P H N I R A G S I K C K A W G A V S A N
V I R S H N S T Q H T S R K H K V S L G C L M S E L
L S A H N S T Q H T S R K H K V S L G C L M S E L
T N D A L E V C C V L R F C L T Y L R P H R I L S S I V

Asel

Pvu II Asel Hae III

CTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCA 1520
GAGTGTAATTAACGCAACGCGAGTGACGGGCGAAAGGTCAGCCCTTTGGACAGCACGGTCGACGTAATTACTTAGCCGGT
L T L I A L R S L P A F Q S G N L S C Q L H I G Q
S H I N C R V A L T A R F P V G K P V V P A A L M N R P
T H I N C R V A L T A R F P V G K P V V P A A L M N R P
S V N I A N R E S G A K W D P F R D H W S C H I P W L
E C M L Q T A S V A R K G T P F G T T G A A N I F R G

Sap I

ACGCGCGGGGAGAGGCGGTTTTCGTATTGGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCCGGC 1600
TGCGCGCCCTCTCCGCCAAACGCATAACCCGCGAGAAGGCGAAGGAGCGAGTGACTGAGCGACGCGAGCCAGCAAGCCG
R A G R G G L R I G R S S A S S L T D S L R S V V R
N A R G E A V C V L G A L P L P R S L T R C A L R S F G
T R G E R R F A Y W A L F P R F L A H L A A L G R S A
R A P L P P K R I P R E E A E E S V S E S R E T T R S
V A R P S L R N A Y Q A S K R K R A Q S A A S P R E A

BsrB I

TGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAATATG 1680
ACGCCGCTCGCCATAGTCGAGTGAGTTTCCGCCATTATGCCAATAGGTGTCTTAGTCCCCTATTGCGTCCTTTCTTGAC
L R R A V S A H S K A V I R L S T E S G D N A G K N M
C A G E R Y Q L T Q R G N Y G Y P Q N Q G I T R Q E R T H
L A A S G I S S L K G G N T V I H R I R G R R K E H
Q P R A T D A E F A T I R N D V S D P S L A P F F M
A A L P I L E S L P P L V T I W L I L P Y R L F S C T

FIG. 18E

28/34

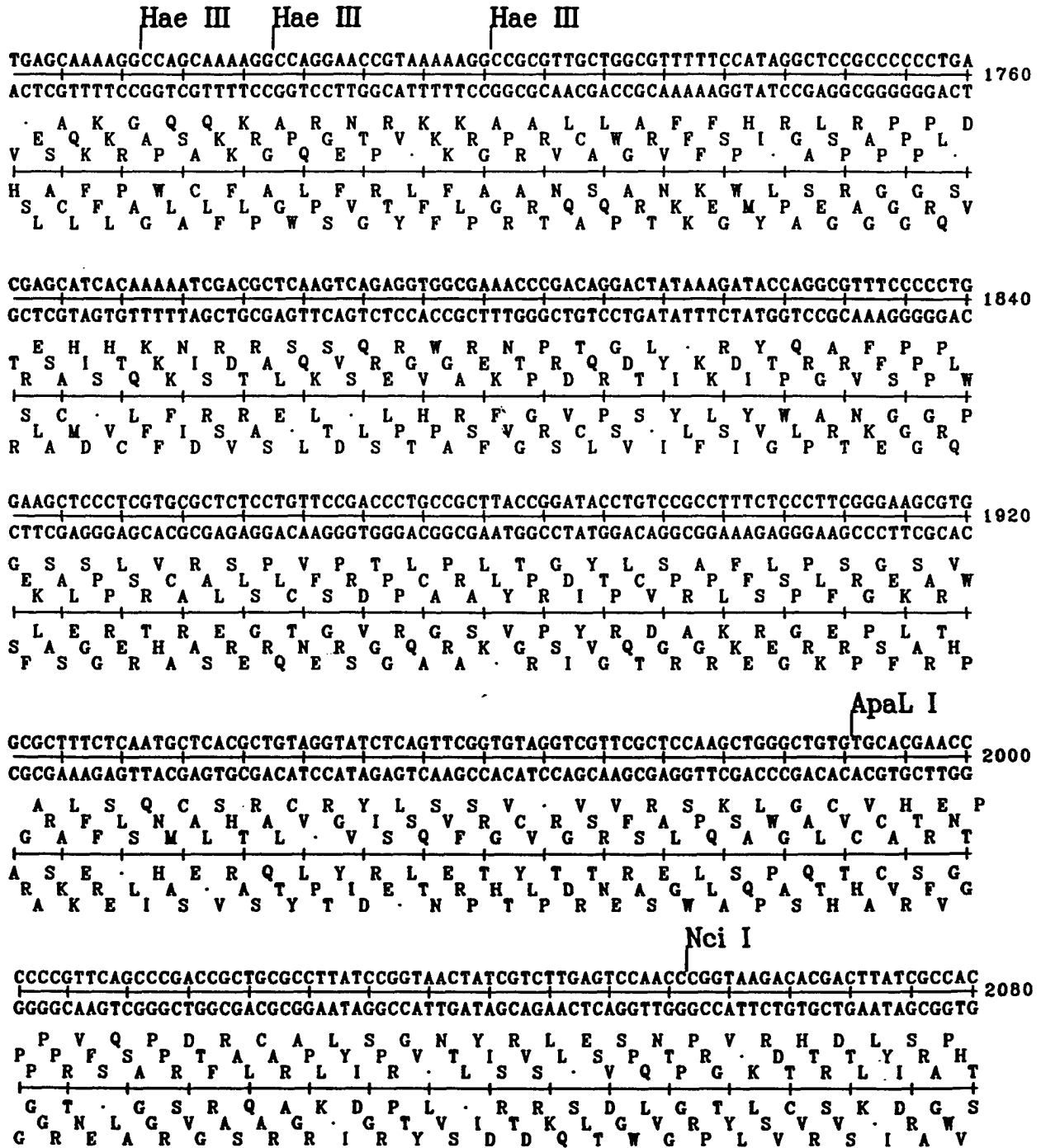


FIG. 18F

29/34

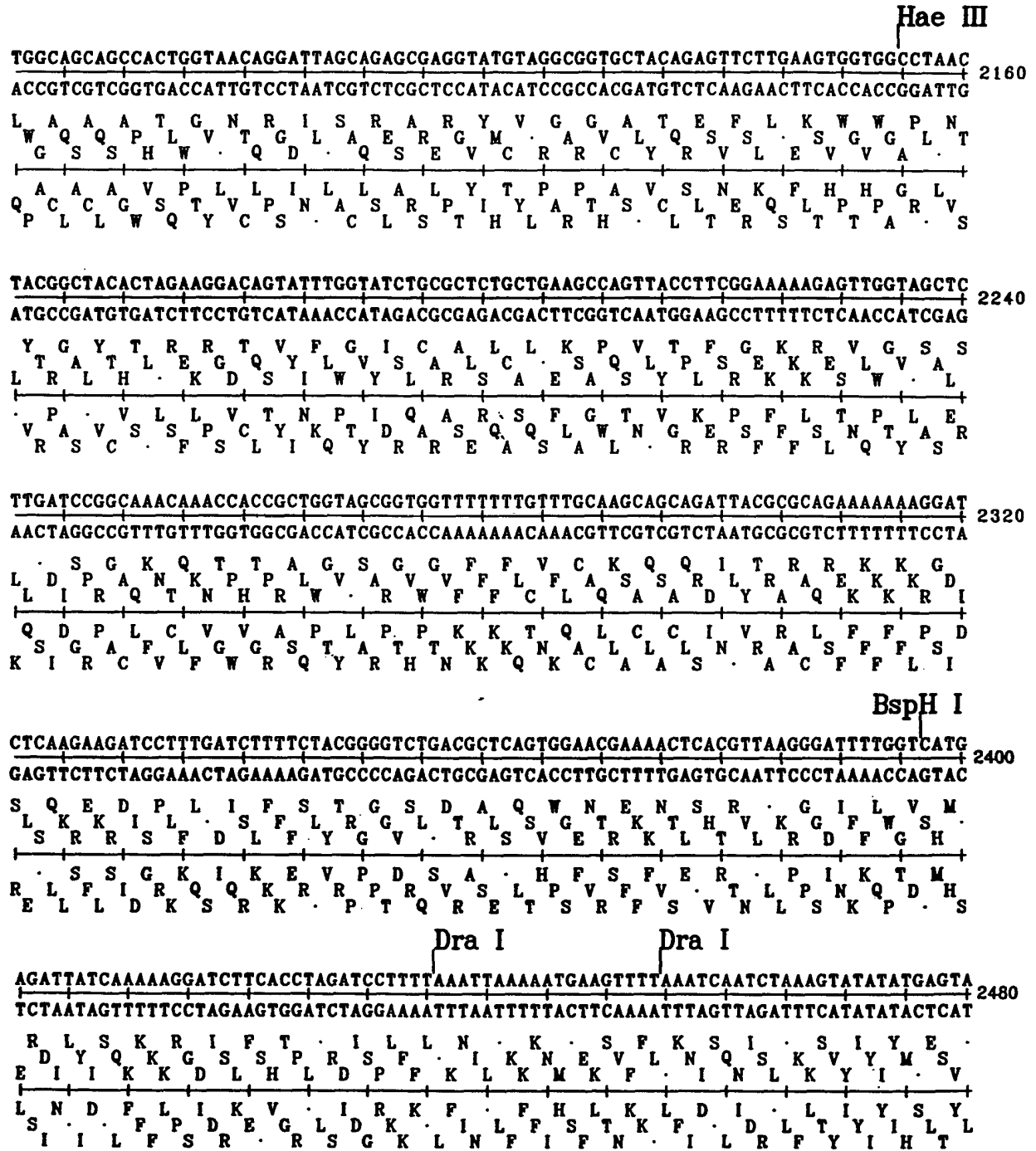


FIG. 18G

30/34

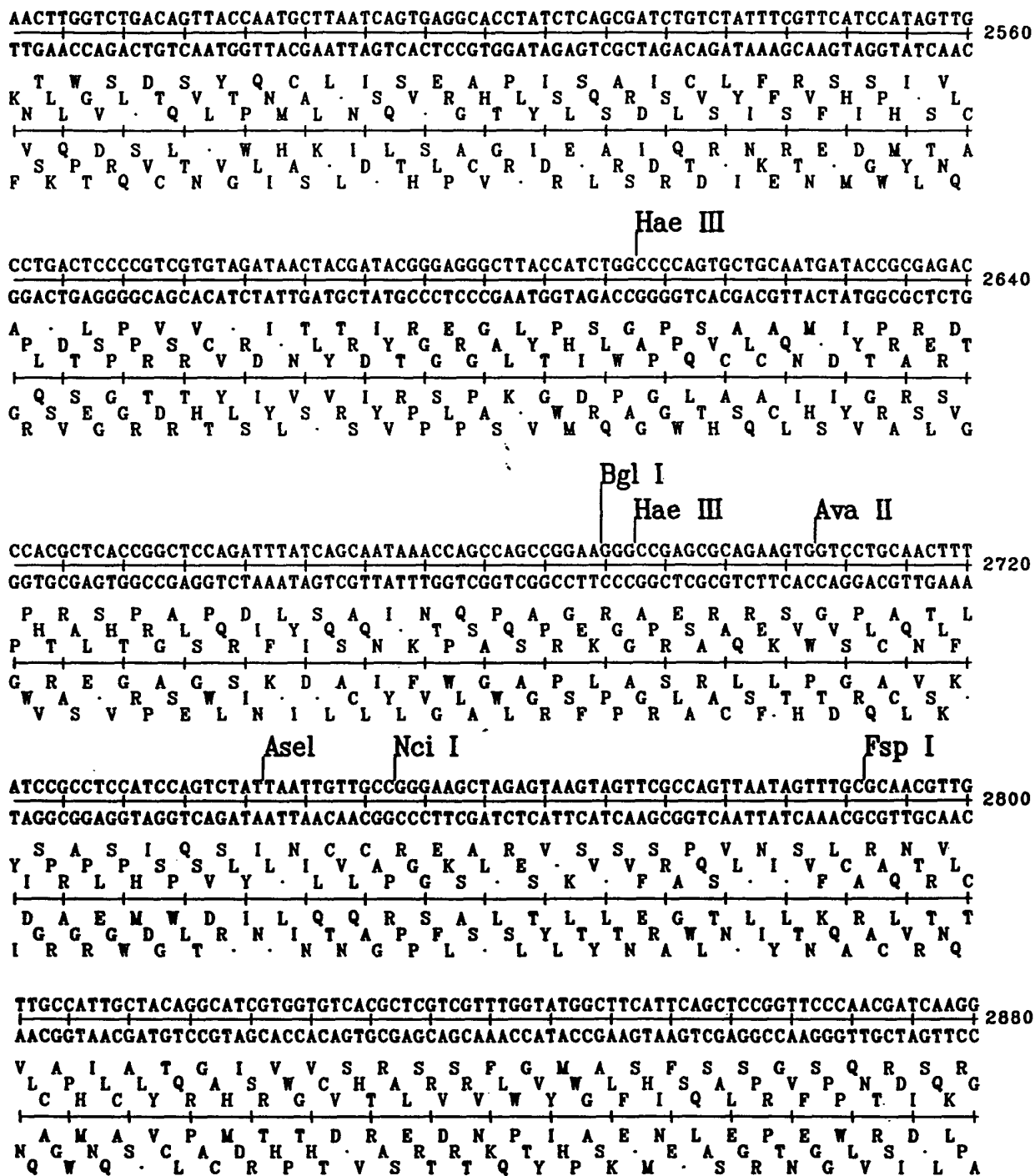


FIG. 18H

31/34

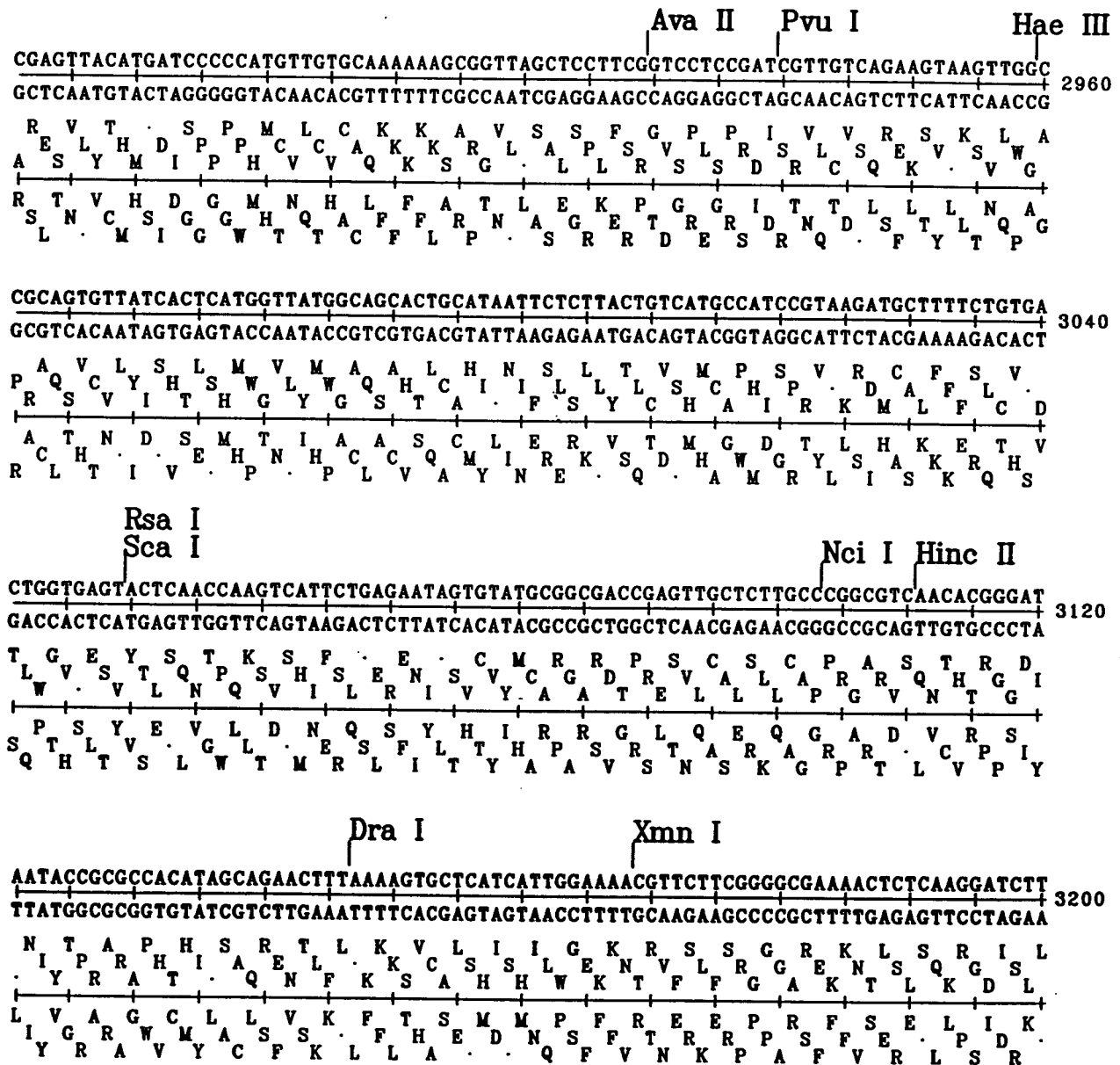


FIG. 18I

32/34

Apal I

ACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTACCAGCGTTT 3280
TGGCGACAACCTCTAGGTCAAGCTACATTGGGTGAGCACGTGGGTGACTAGAAAGTCGTAGAAAATGAAAGTGGTCGCAAA
P L L R S S S M P T R A P N S S A S F T F T S V
Y R C D P V R C N P L V H P T D L Q H L F L S P A F
T A V E I Q F D V T H S C T Q L I F S I F Y F H Q R F
G S N L D L E I Y G V R A G L Q D E A D K V K V L T E
V R Q T S I G W N S T V W E H V W S I K L M K K W R K

CTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTC 3360
GACCCACTCGTTTTGTCTTCCGTTTTACGGCGTTTTTCCCTTATTCCCGCTGTGCCTTTACAACCTTATGAGTATGAG
S G A K T G R Q N A A K K G I R A T R K C I L I L
L G E Q K Q E G K M P Q K K R G N K G G D T E N V L E Y S Y S
W V S K N R K A K C R K K G N K G G D T E N V L E Y S Y S
P H A F V P L C F A A F F P I L A V R F H Q I S M S
R P S C F C S P L I G C F L S Y P R C P F T Q I Y E Y E
Q T L L F L F A F H R L F P F L P S V S I N F V V E R

Hinc II

Spe I Asel

TTCCTTTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCTCATGCGCGTTGACATTGATTATTGACTAGTTATTAA 3440
AAGGAAAAAGTTATAATAAATTCTGTAATAGTCCCAATAACAGAGTACGCGCAACTGTAACATAAATACTGATCAATAATT
F L F Q Y Y S I Y Q G Y C L M R V D I D Y L V I N
L P F S I L L K H L S G L Y S H A R H L L T S Y L
K R K Y Q L M P Q R M R T S V M S I S T N I L
E K K L I I S A N I L T I T E H A R Q C Q N N V L N I
G K E I N N F C K D P N N D A R Q C Q N N V L N I

Hae III

Bgl I

TAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGGCGTTACATAAATTACGGTAATGGCCCGCC 3520
ATCATTAGTTAATGCCCCAGTAATCAAGTATCGGGTATATACCTCAAGGCGCAATGTATTGAATGCCATTTACGGGGCGG
S N Q L R G H F I A H I W S S A L H N L R M A P
I V I N Y G V I S F I P I Y G V P R Y I T Y G K W P A
L S I T G S L V H S P Y M E F R V T L T V N G P P
L L N R P T M N M A W I H L E A N C L K R Y I A R R
Y Y D I V P D N T L G Y I S N R T V Y S V T F P G A G

FIG. 18J

33/34

Aat II
TGGCTGACCGCCCAACGACCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCC 3600
ACCGACTGGCGGGTGTCTGGGGGCGGGTAAGTGCAGTTATTACTGCATACAAGGGTATCATTGCGGTTATCCCTGAAAGG
L A D R P T T P A H R V Q N N D R V C S P H S N A Q R G L S P
W L T A P Q N D P P P L T S I M T Y V S P I V T P I G T F P
G P P N D P R P L T S I M T Y V S P I V T P I G T F P
A S R G V V G A W Q R Y H R I N G Y Y R W Y P S K E
Q S V A W R G G G M S T L L S T H E W L L A L L S K G
P Q G G L S G R G N V D I I V Y T G M T V G I P V K W

Aat II Bgl I Rsa I Nde I Rsa I
ATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCC 3680
TAACTGCAGTTACCCACCTGATAAATGCCATTGACGGGTGAACCGTCATGTAGTTCACATAGTATACGGTTCATGCGGG
I D V N G W T I Y G K L P T W Q Y I K C I I C Q V R P
L T S M G G L F T V N C P L G S T S K V S Y A K Y A P
H R Q W V D Y L R T A H L A V H Q V Y H M P S T P
M S T L P H V I P L S G V Q C Y M L H I M H W T Y R G
N V D I P P S N V T F A G S P L V D L T D Y A L Y A G
Q R H T S K R Y V A W K A T C T Y I G L V G

Aat II Hae III Bgl I Rsa I
CCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCACTACATGACCTTATGGGACTTTCTACTTGGCA 3760
GGATAACTGCAGTTACTGCCATTACCGGGCGGACCGTAATACGGGTCACTGACTGGAATACCCTGAAAGGATGAACCGT
L L T S M T V N G P P G I M P S T P Y G T F L L G
P Y R Q N D G K W P A W H Y A Q Y M T L W D F P T W Q
R N V D I V T F P G G P M I G L V H G P V K R S P L
G I S T L S P L H G A Q A C A W Y M V K H S K G V Q A C

BsaA I Nco I Rsa I
Rsa I SnaB I Sty I
GTACATCTACGTATTAGTCATCGCTATTACCATGGTATGCGGTTTTGGCAGTACATCAATGGCGGTGGATAGCGGTTTG 3840
CATGTAGATGCATAATCAGTAGCGATAATGGTACCCTACGCCAAAACCGTCATGTAGTTACCCGCACCTATCGCCAAAC
S T S T Y S S L L P W C G F G S T S M G V D S G L
V H L R I S H R Y Y H G D A V L A V H Q W A W I A V
Y I Y V L V I A I T M V M R F W Q Y I N G R G R F
V D V Y D D S N G H H H P K P L V D I P T S L P K
T Y C R R I L R A I V M T I R N Q C Y M L P R P Y R N S

FIG. 18K

